

FIGURE 1

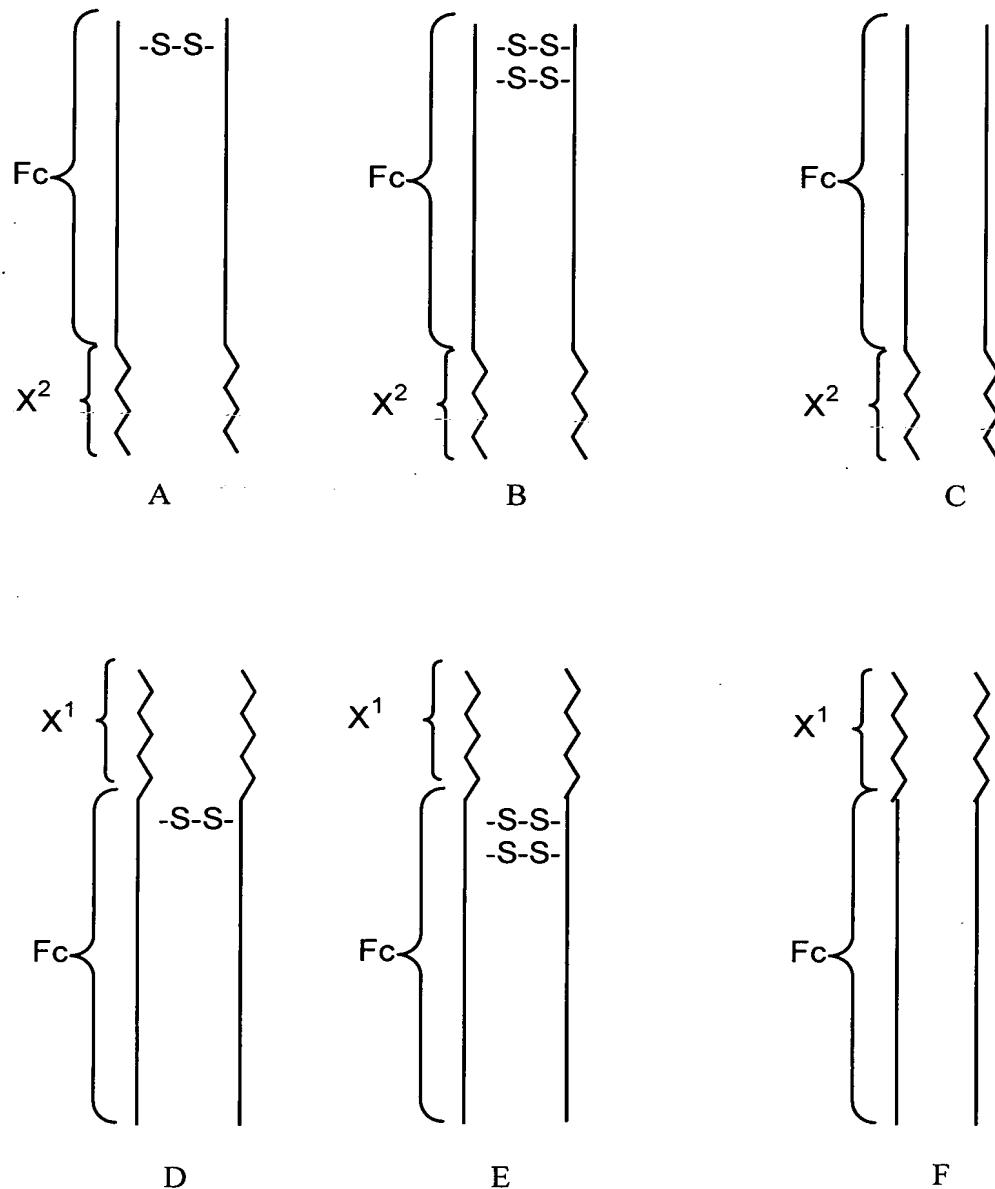


FIGURE 2

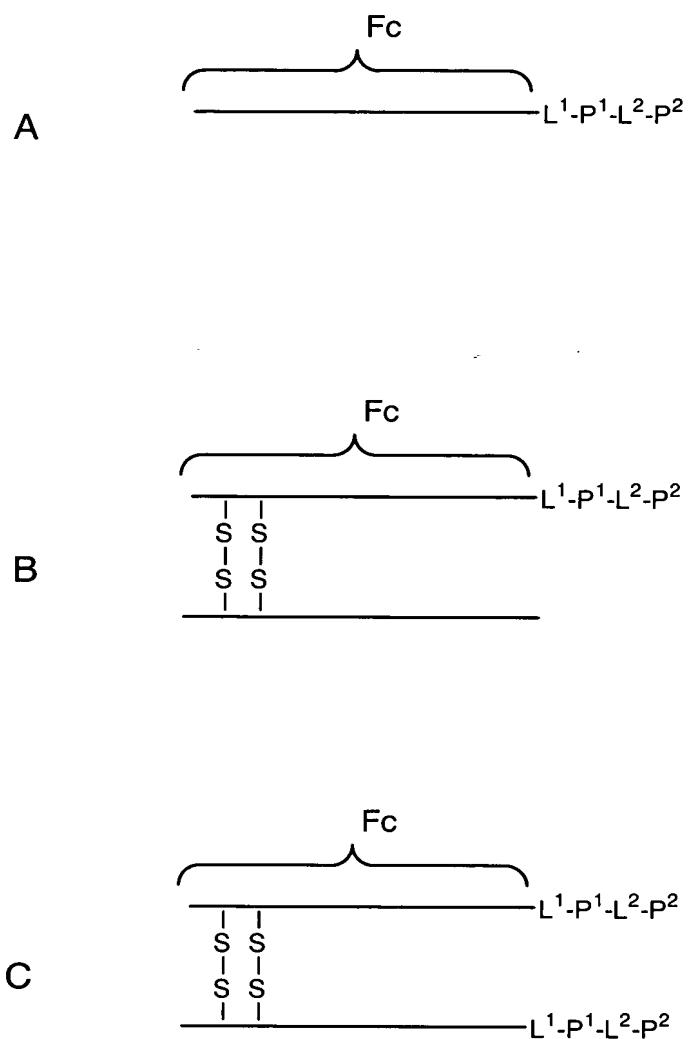


FIGURE 3A

ATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCGTCA
 1 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
 TACCTGTTTGAGTGTACAGGTGGAACAGGTGAGGCTTGAGGACCCCCCTGGCAGT

 a M D K T H T C P P C P A P E L L G G P S -

 GTCTTCCTCTCCCCAAAACCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTC
 61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
 CAGAAGGAGAAGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGACTCCAG

 a V F L F P P K P K D T L M I S R T P E V -

 ACATGCGTGGTGGACGTGAGGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTG
 121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
 TGTACGCACCACCTGCACTCGGTGCTTCTGGACTCCAGTTCAAGTTGACCATGCAC

 a T C V V V D V S H E D P E V K F N W Y V -

 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
 181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
 CTGCCGCACCTCCACGTATTACGGTTCTGTTCGGCGCCCTCTCGTCATGTTGCGTGC

 a D G V E V H N A K T K P R E E Q Y N S T -

 TACCGTGTGGTCAGCGTCCTCACCGTCTGCAACCAGGACTGGCTGAATGGCAAGGAGTAC
 241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
 ATGGCACACCAGTCGCAAGGAGTGGCAGGACGTGGCCTGACCGACTTACCGTCCATG

 a Y R V V S V L T V L H Q D W L N G K E Y -

 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACATCTCCAAAGCC
 301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
 TTCACGTTCCAGAGGTTCTCGGGAGGGTCGGGGTAGCTCTTGGTAGAGGTTTCGG

 a K C K V S N K A L P A P I E K T I S K A -

 AAAGGGCAGCCCCGAGAACCAACAGGTGTACACCCCTGCCCGGATGAGCTGACC
 361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
 TTTCCCGTCGGGCTCTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGG

 a K G Q P R E P Q V Y T L P P S R D E L T -

 AAGAACCCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATGCCGTG
 421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
 TTCTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGTCGCTGTAGCGGCAC

 a K N Q V S L T C L V K G F Y P S D I A V -

 GAGTGGGAGAGCAATGGGAGCCGGAGAACAAACTACAAGAACACGCCCTCCGTGGAC
 481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
 CTCACCCCTCTCGTTACCGTCGGCCTTGTGATGTTCTGGTGCAGGGCACGACCTG

 a E W E S N G Q P E N N Y K T T P P V L D -

 TCCGACGGCTCCTCTTCCCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAG
 541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
 AGGCTGCCAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCCTCG

 a S D G S F F L Y S K L T V D K S R W Q Q -

 GGGAACGTCTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACCAACTACACGCAGAAG
 601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
 CCCTTGAGAAGAGTACGAGGCACACTGTAACGACTCCGAGACGTGTTGGTATGTGCGCTTC

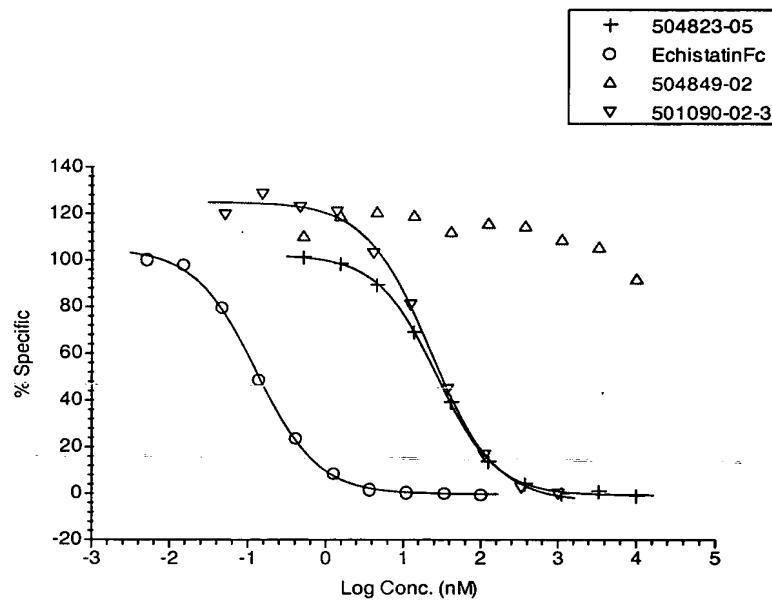
 a G N V F S C S V M H E A L H N H Y T Q K -

FIGURE 3B

661 AGCCTCTCCCTGTCTCCGGGTAAA 684
661 -----+-----+----- 684
TCGGAGAGGGACAGAGGCCATT
a S L S L S P G K

FIGS. 4A and 4B

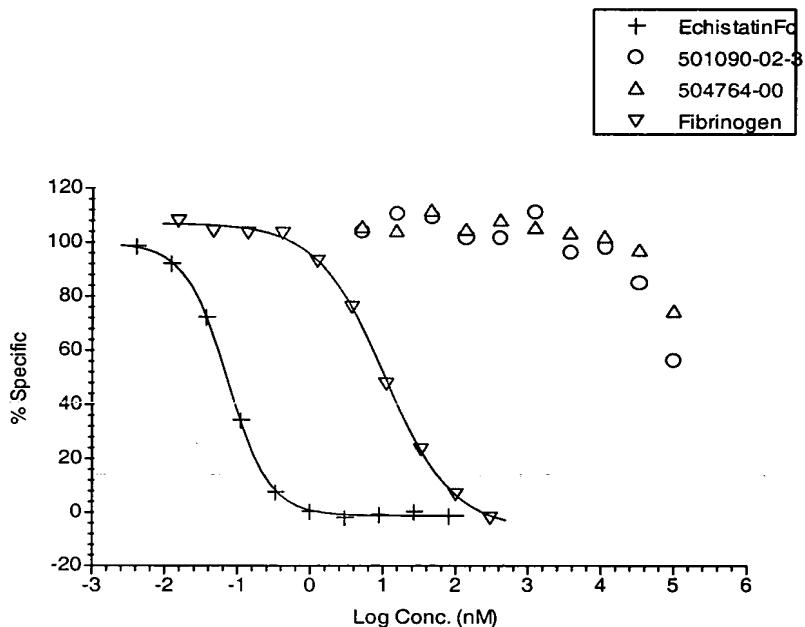
Inhibition of hu Vitronectin-Ru Binding to $\alpha\beta 3$



Conc.	IC50 IP	Hill Slope	r2	Ki
AMG 504823-05	26.73786	-1.14	1.000	21.10884
AMG EchistatinFc	0.12722	-1.10	0.999	0.10044
AMG 504849-02	>10000			>10000
AMG 501090-02-3	22.33247	-1.04	0.997	17.63090

FIGS. 5A and 5B

Inhibition of hu Fibrinogen-Ru Binding To



nM

Conc.	IC50 IP	r2	Ki
AMG EchistatinFc	0.07187	1.000	0.03594
AMG 501090-02-3	>100000		>100000
AMG 504764-00	>100000		>100000
AMG Fibrinogen	10.51409	0.999	5.25705